



SEQUENCE LISTING

<110> SHERMAN, LINDA A.
LUSTGARTEN, JOSEPH

<120> RECOMBINANT CONSTRUCTS ENCODING T CELL RECEPTORS
SPECIFIC FOR HUMAN HLA-RESTRICTED TUMOR ANTIGENS

<130> 46147/55793

<140> 08/812,393

<141> 1997-03-05

<160> 64

<170> PatentIn Ver. 2.1

<210> 1

<211> 1350

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(1332)

<220>

<223> Description of Artificial Sequence: Synthetic
single chain TCR derivative nucleotide sequence

<400> 1

ctc	gag	atg	cag	agg	aac	ctg	gga	gct	gtg	ctg	ggg	att	ctg	tgg	gtg	48
Leu	Glu	Met	Gln	Arg	Asn	Leu	Gly	Ala	Val	Leu	Gly	Ile	Leu	Trp	Val	
1				5					10					15		

cag	att	tgc	tgg	ctg	aaa	gaa	cag	caa	gtg	cag	cag	agt	ccc	gca	tcc	96
Gln	Ile	Cys	Trp	Leu	Lys	Glu	Gln	Gln	Val	Gln	Gln	Ser	Pro	Ala	Ser	
		20					25						30			

ttg	gtt	ctg	cag	gag	ggg	gag	aac	gca	gag	ctc	cag	tgt	agc	ttt	tcc	144
Leu	Val	Leu	Gln	Glu	Gly	Glu	Asn	Ala	Glu	Leu	Gln	Cys	Ser	Phe	Ser	
	35					40						45				

atc	ttt	aca	aac	cag	gtg	cag	tgg	ttt	tac	caa	cgt	cct	ggg	gga	aga	192
Ile	Phe	Thr	Asn	Gln	Val	Gln	Trp	Phe	Tyr	Gln	Arg	Pro	Gly	Gly	Arg	
	50				55				60							

ctc	gtc	agc	ctg	ttg	tac	aat	cct	tct	ggg	aca	aag	cag	agt	ggg	aga	240
Leu	Val	Ser	Leu	Leu	Tyr	Asn	Pro	Ser	Gly	Thr	Lys	Gln	Ser	Gly	Arg	
65				70					75					80		

ctg	aca	tcc	aca	aca	gtc	att	aaa	gaa	cgt	cgc	agc	tct	ttg	cac	att	288
Leu	Thr	Ser	Thr	Thr	Val	Ile	Lys	Glu	Arg	Arg	Ser	Ser	Leu	His	Ile	
			85				90						95			

tcc	tcc	tcc	cag	atc	aca	gac	tca	ggc	act	tat	ctc	tgt	gcc	tca	aat	336
Ser	Ser	Ser	Gln	Ile	Thr	Asp	Ser	Gly	Thr	Tyr	Leu	Cys	Ala	Ser	Asn	
			100				105						110			

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2

tct gga gga agc aat gca aag cta acc ttc ggg aaa ggc act aaa ctg	384
Ser Gly Gly Ser Asn Ala Lys Leu Thr Phe Gly Lys Gly Thr Lys Leu	
115 120 125	
tct gtt aaa tca ggt ggc gga ggg tct ggc ggg ggt gga tcc ggg ggt	432
Ser Val Lys Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly	
130 135 140	
gga ggc tca gag gct gca gtc acc caa agc cca aga aac aag gtg gca	480
Gly Gly Ser Glu Ala Ala Val Thr Gln Ser Pro Arg Asn Lys Val Ala	
145 150 155 160	
gta aca gga gga aag gtg aca ttg agc tgt aat cag act aat aac cac	528
Val Thr Gly Gly Lys Val Thr Leu Ser Cys Asn Gln Thr Asn Asn His	
165 170 175	
aac aac atg tac tgg tat cgg cag gac acg ggg cat ggg ctg agg ctg	576
Asn Asn Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu	
180 185 190	
atc cat tat tca tat ggt gct ggc agc act gag aaa gga gat atc cct	624
Ile His Tyr Ser Tyr Gly Ala Gly Ser Thr Glu Lys Gly Asp Ile Pro	
195 200 205	
gat gga tac aag gcc tcc aga cca agc caa gag aac ttc tcc ctg att	672
Asp Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu Asn Phe Ser Leu Ile	
210 215 220	
ctg gag ttg gct acc ccc tct cag aca tca gtg tac ttc tgt gcc agc	720
Leu Glu Leu Ala Thr Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser	
225 230 235 240	
ggt gag aca ggg acc aac gaa aga tta ttt ttc ggt cat gga acc aag	768
Gly Glu Thr Gly Thr Asn Glu Arg Leu Phe Phe Gly His Gly Thr Lys	
245 250 255	
ctg tct gtc ctg act agt aac tcc atc atg tac ttc agc cac ttc gtg	816
Leu Ser Val Leu Thr Ser Asn Ser Ile Met Tyr Phe Ser His Phe Val	
260 265 270	
ccg gtc ttc ctg cca gcg aag ccc acc acg acg cca gcg ccg cga cca	864
Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro	
275 280 285	
cca aca ccg gcg ccc acc atc gcg tcg cag ccc ctg tcc ctg cgc cca	912
Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro	
290 295 300	
tct agt tct aga gat ccc aaa ctg tgc tac ctg ctg gat gga atc ctg	960
Ser Ser Ser Arg Asp Pro Lys Leu Cys Tyr Leu Leu Asp Gly Ile Leu	
305 310 315 320	
ttc atc tat ggt gtc att ctg act gcc ttg ttc ctg aga gtg aag ttc	1008
Phe Ile Tyr Gly Val Ile Leu Thr Ala Leu Phe Leu Arg Val Lys Phe	
325 330 335	

agc agg agc gca gac gcc ccc gcg tac cag cag ggc cag aac cag ctc 1056
 Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
 340 345 350
 tat aac gag ctc aat cta gga cga aga gag gag tac gat gtt ttg gac 1104
 Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
 355 360 365
 aag aga cgt ggc cgg gac cct gag atg ggg gga aag ccg aga agg aag 1152
 Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
 370 375 380
 aac cct cag gaa ggc ctg tac aat gaa ctg cag aaa gat aag atg gcg 1200
 Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
 385 390 395 400
 gag gcc tac agt gag att ggg atg aaa ggc gag cgc cgg agg ggc aag 1248
 Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
 405 410 415
 ggg cac gat ggc ctt tac cag ggt ctc agt aca gcc acc aag gac acc 1296
 Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
 420 425 430
 tac gac gcc ctt cac atg cag gcc ctg ccc cct cgc taa gcg gcc gcc 1344
 Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
 435 440
 acc gcg 1350

<210> 2

<211> 444

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
single chain TCR protein

<400> 2

Leu Glu Met Gln Arg Asn Leu Gly Ala Val Leu Gly Ile Leu Trp Val
 1 5 10 15
 Gln Ile Cys Trp Leu Lys Glu Gln Gln Val Gln Gln Ser Pro Ala Ser
 20 25 30
 Leu Val Leu Gln Glu Gly Glu Asn Ala Glu Leu Gln Cys Ser Phe Ser
 35 40 45
 Ile Phe Thr Asn Gln Val Gln Trp Phe Tyr Gln Arg Pro Gly Gly Arg
 50 55 60
 Leu Val Ser Leu Leu Tyr Asn Pro Ser Gly Thr Lys Gln Ser Gly Arg
 65 70 75 80
 Leu Thr Ser Thr Thr Val Ile Lys Glu Arg Arg Ser Ser Leu His Ile
 85 90 95

Ser Ser Ser Gln Ile Thr Asp Ser Gly Thr Tyr Leu Cys Ala Ser Asn
 100 105 110
 Ser Gly Gly Ser Asn Ala Lys Leu Thr Phe Gly Lys Gly Thr Lys Leu
 115 120 125
 Ser Val Lys Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
 130 135 140
 Gly Gly Ser Glu Ala Ala Val Thr Gln Ser Pro Arg Asn Lys Val Ala
 145 150 155 160
 Val Thr Gly Gly Lys Val Thr Leu Ser Cys Asn Gln Thr Asn Asn His
 165 170 175
 Asn Asn Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu
 180 185 190
 Ile His Tyr Ser Tyr Gly Ala Gly Ser Thr Glu Lys Gly Asp Ile Pro
 195 200 205
 Asp Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu Asn Phe Ser Leu Ile
 210 215 220
 Leu Glu Leu Ala Thr Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser
 225 230 235 240
 Gly Glu Thr Gly Thr Asn Glu Arg Leu Phe Phe Gly His Gly Thr Lys
 245 250 255
 Leu Ser Val Leu Thr Ser Asn Ser Ile Met Tyr Phe Ser His Phe Val
 260 265 270
 Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro
 275 280 285
 Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
 290 295 300
 Ser Ser Ser Arg Asp Pro Lys Leu Cys Tyr Leu Leu Asp Gly Ile Leu
 305 310 315 320
 Phe Ile Tyr Gly Val Ile Leu Thr Ala Leu Phe Leu Arg Val Lys Phe
 325 330 335
 Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
 340 345 350
 Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
 355 360 365
 Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
 370 375 380
 Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
 385 390 395 400

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
 405 410 415

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
 420 425 430

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
 435 440

<210> 3

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 3

cccaaggcac tgatgttcat cttc

24

<210> 4

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 4

tgagacaaag tccccaatct ctgacag

27

<210> 5

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 5

ctgcagctgc tcctcaagta ctattc

26

<210> 6

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 6

tcccggagaa ggtccacagt tcctcttt

28

<210> 7
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 7
gaagcagcag agggtttgaa gccacatac

29

<210> 8
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 8
ggcaggtctt cagttgctta tgaaggt

27

<210> 9
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 9
ggttcctctt cagggtccag aatatgt

27

<210> 10
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 10
gcgaagaact caccctggac tgttcat

27

<210> 11
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 11
gagctccaca gacaacaaga ggacgcagca

30

<210> 12
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 12
gagctgcgac gttccttagt gactgtg 27

<210> 13
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 13
cctcgtcagc ctgttggtcca atccttctgg 30

<210> 14
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 14
cagcctcctc aatctgttct acttggt 28

<210> 15
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 15
ccaccaggga ccacagtta tcattcaa 28

<210> 16
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 16
acctggagag aatcctaagc tcatcat 27

<210> 17
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 17
aggtcttgtg tccctgacag tctctggt 28

<210> 18
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 18
caagcaaaca ctgtagtgca gagcccttcc 30

<210> 19
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 19
caagacatcc ataactgccc tacag 25

<210> 20
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 20
gtgtatgaaa cccaggacag ttcttac 27

<210> 21
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 21
ccgtatttct ttcttatggt gttttggat 29

<210> 22
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 22
caaagctctc catcgctgac tgttcaag 28

<210> 23
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 23
atctaatacct gggaagagca aat 23

<210> 24
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 24
ggcgtctggt accacgtggt caa 23

<210> 25
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 25
gtgaaagggc aaggacaaaa agc 23

<210> 26
<211> 22

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 26
gatatgCGaa cagtatctag gc 22

<210> 27
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 27
acataatcaa aggaaaggga gaa 23

<210> 28
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 28
tcctgattgg tcaggaaggg caa 23

<210> 29
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 29
tacctgatca aaagaatggg aga 23

<210> 30
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 30
ataaccatga caatatgtac tgg 23

<210> 31
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 31
ataaccacaa caacatgtac tgg 23

<210> 32
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 32
atagccacaa ctacatgtac tgg 23

<210> 33
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 33
agcttgcaag agttggaaaa cca 23

<210> 34
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 34
gattatgttt agctacaata ata 23

<210> 35
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 35
acaagggtgac agggaaggga caa 23

<210> 36
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 36
acctacagaa cccaaggact cag 23

<210> 37
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 37
cagttgcct cggatcgatt ttc 23

<210> 38
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 38
gccgagatca aggtgtggg cag 23

<210> 39
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 39
agaaccatct gtaagagtg aac 23

<210> 40
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 40
catcaaataa tagatatggg gca

23

<210> 41
<211> 23
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 41
gtagtctga aaaagggcac act

23

<210> 42
<211> 22
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 42
catctgtcaa agtggcactt ca

22

<210> 43
<211> 393
<212> DNA
<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(393)

<400> 43
atg aaa tcc ttg agt gtt tcc cta gtg gtc ctg tgg ctc cag tta aac 48
Met Lys Ser Leu Ser Val Ser Leu Val Val Leu Trp Leu Gln Leu Asn
1 5 10 15
tgg gtg cag agc cag cag aag gtg cag cag agc cca gaa tcc ctc agt 96
Trp Val Gln Ser Gln Gln Lys Val Gln Gln Ser Pro Glu Ser Leu Ser
20 25 30
gtc cca gag gga ggc atg gcc tct ctc aac tgc act tca agt gat cgc 144
Val Pro Glu Gly Gly Met Ala Ser Leu Asn Cys Thr Ser Ser Asp Arg
35 40 45
aat ttt cag tat ttc tgg tgg tac aga cag cat tct gga gaa ggc ccc 192
Asn Phe Gln Tyr Phe Trp Trp Tyr Arg Gln His Ser Gly Glu Gly Pro
50 55 60
aaa gca ctg atg tcc atc ttc tct gat ggt gac aag aaa gaa ggc aga 240
Lys Ala Leu Met Ser Ile Phe Ser Asp Gly Asp Lys Lys Glu Gly Arg
65 70 75 80

ttc aca gct cac ctc aat aag gcc agc ctg cat gtt tcc ctg cac atc 288
 Phe Thr Ala His Leu Asn Lys Ala Ser Leu His Val Ser Leu His Ile
 85 90 95

 aga gac tcc cag ccc agt gac tcc gct ctc tac ttc tgt gca gtt atg 336
 Arg Asp Ser Gln Pro Ser Asp Ser Ala Leu Tyr Phe Cys Ala Val Met
 100 105 110

 gat tat aac cag ggg aag ctt atc ttt ggg cag ggt acc aag tta tct 384
 Asp Tyr Asn Gln Gly Lys Leu Ile Phe Gly Gln Gly Thr Lys Leu Ser
 115 120 125

 atc aag ccc 393
 Ile Lys Pro
 130

<210> 44
 <211> 131
 <212> PRT
 <213> Homo sapiens

<400> 44
 Met Lys Ser Leu Ser Val Ser Leu Val Val Leu Trp Leu Gln Leu Asn
 1 5 10 15

 Trp Val Gln Ser Gln Gln Lys Val Gln Gln Ser Pro Glu Ser Leu Ser
 20 25 30

 Val Pro Glu Gly Gly Met Ala Ser Leu Asn Cys Thr Ser Ser Asp Arg
 35 40 45

 Asn Phe Gln Tyr Phe Trp Trp Tyr Arg Gln His Ser Gly Glu Gly Pro
 50 55 60

 Lys Ala Leu Met Ser Ile Phe Ser Asp Gly Asp Lys Lys Glu Gly Arg
 65 70 75 80

 Phe Thr Ala His Leu Asn Lys Ala Ser Leu His Val Ser Leu His Ile
 85 90 95

 Arg Asp Ser Gln Pro Ser Asp Ser Ala Leu Tyr Phe Cys Ala Val Met
 100 105 110

 Asp Tyr Asn Gln Gly Lys Leu Ile Phe Gly Gln Gly Thr Lys Leu Ser
 115 120 125

 Ile Lys Pro
 130

<210> 45
 <211> 402
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> (1)...(402)

<400> 45

atg	ggc	tcc	aga	ctc	ttc	ttt	gtg	ggt	ttg	att	ctc	ctg	tgt	gca	aaa	48
Met	Gly	Ser	Arg	Leu	Phe	Phe	Val	Val	Leu	Ile	Leu	Leu	Cys	Ala	Lys	
1				5					10					15		

cac	atg	gag	gct	gca	gtc	acc	caa	agt	cca	aga	agc	aag	gtg	gca	gta	96
His	Met	Glu	Ala	Ala	Val	Thr	Gln	Ser	Pro	Arg	Ser	Lys	Val	Ala	Val	
		20						25					30			

aca	gga	gga	aag	gtg	aca	ttg	agc	tgt	cac	cag	act	aat	aac	cat	gac	144
Thr	Gly	Gly	Lys	Val	Thr	Leu	Ser	Cys	His	Gln	Thr	Asn	Asn	His	Asp	
	35						40					45				

tat	atg	tac	tgg	tat	cgg	cag	gac	acg	ggg	cat	ggg	ctg	agg	ctg	atc	192
Tyr	Met	Tyr	Trp	Tyr	Arg	Gln	Asp	Thr	Gly	His	Gly	Leu	Arg	Leu	Ile	
	50				55						60					

cat	tac	tca	tat	gtc	gct	gac	agc	acg	gag	aaa	gga	gat	atc	cct	gat	240
His	Tyr	Ser	Tyr	Val	Ala	Asp	Ser	Thr	Glu	Lys	Gly	Asp	Ile	Pro	Asp	
65				70						75				80		

ggg	tac	aag	gcc	tcc	aga	cca	agc	caa	gag	aat	ttc	tct	ctc	att	ctg	288
Gly	Tyr	Lys	Ala	Ser	Arg	Pro	Ser	Gln	Glu	Asn	Phe	Ser	Leu	Ile	Leu	
		85						90						95		

gag	ttg	gct	tcc	ctt	tct	cag	tca	gct	gta	tat	ttc	tgt	gcc	agc	agc	336
Glu	Leu	Ala	Ser	Leu	Ser	Gln	Ser	Ala	Val	Tyr	Phe	Cys	Ala	Ser	Ser	
	100							105					110			

gat	ttc	gcc	ggg	aca	ggg	ggc	ttc	tat	gaa	cag	tac	ttc	ggg	ccc	ggc	384
Asp	Phe	Ala	Gly	Thr	Gly	Gly	Phe	Tyr	Glu	Gln	Tyr	Phe	Gly	Pro	Gly	
	115						120					125				

acc	agg	ctc	acg	gtt	tct											402
Thr	Arg	Leu	Thr	Val	Ser											
	130															

<210> 46

<211> 134

<212> PRT

<213> Homo sapiens

<400> 46

Met	Gly	Ser	Arg	Leu	Phe	Phe	Val	Val	Leu	Ile	Leu	Leu	Cys	Ala	Lys
1				5					10					15	

His	Met	Glu	Ala	Ala	Val	Thr	Gln	Ser	Pro	Arg	Ser	Lys	Val	Ala	Val
		20						25					30		

Thr	Gly	Gly	Lys	Val	Thr	Leu	Ser	Cys	His	Gln	Thr	Asn	Asn	His	Asp
	35						40					45			

Tyr Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu Ile
 50 55 60
 His Tyr Ser Tyr Val Ala Asp Ser Thr Glu Lys Gly Asp Ile Pro Asp
 65 70 75 80
 Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu Asn Phe Ser Leu Ile Leu
 85 90 95
 Glu Leu Ala Ser Leu Ser Gln Ser Ala Val Tyr Phe Cys Ala Ser Ser
 100 105 110
 Asp Phe Ala Gly Thr Gly Gly Phe Tyr Glu Gln Tyr Phe Gly Pro Gly
 115 120 125
 Thr Arg Leu Thr Val Ser
 130

<210> 47
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 47
 Lys Ile Phe Gly Ser Leu Ala Phe Leu
 1 5

<210> 48
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 48
 Thr Leu Gln Gly Leu Gly Ile Ser Trp Leu
 1 5 10

<210> 49
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 49

Val Met Ala Gly Val Gly Ser Pro Tyr Val
1 5 10

<210> 50

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 50

Val Leu Gln Gly Leu Pro Arg Glu Tyr Val
1 5 10

<210> 51

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

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His Leu Tyr Gln Gly Cys Gln Val Val
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